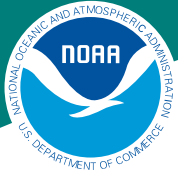


Genetic Stock Identification (GSI) of Pacific Salmon

2011



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How do we distinguish individuals from different stocks of fish?

In order to identify risks and develop recovery actions for Pacific salmon, resource managers typically focus on specific stocks of fish. However, stock-specific management actions can be difficult to implement since groups of fish are often mixtures of stocks from different areas or with different behaviors. This presents a particular challenge for decision-makers seeking to balance fishing opportunities with resource conservation when abundant stocks intermingle with weaker stocks.

GSI is one of the most successful biological tools to determine composition of mixed stocks and origin of individual fish.

A variety of identification methods are utilized to analyze mixtures of fish in an effort to study or benefit specific spawning populations of salmon. While some methods artificially place a tag on a fish, other methods such as GSI take advantage of the naturally-occurring, inherent biological differences between stocks.

The advantages of modern GSI include:

- Conceptually, all stocks are “marked”, including ESA-listed wild stocks.
- Fish can be easily and non-lethally sampled.
- Tissue samples require no special storage.
- Can provide close to “real-time” information on stock composition.
- Estimates are based on a solid statistical framework.

The NWFSC has a long history of using GSI to conduct research on Pacific salmon.

Over the past 30 years, the Northwest Fisheries Science Center (NWFSC) has emerged as a nationally-recognized leader in the field of conservation genetics. In the 1970s, the NWFSC pioneered the use of proteins to determine the genetic differences among mixed stocks. Today, we utilize DNA microsatellite markers and single nucleotide polymorphisms (SNP) to dramatically increase the power of GSI and add the capability of assigning individual fish to their likely population of origin.

Current GSI Studies at NWFSC

The NWFSC’s extensive collaborations with agencies and universities have resulted in several baseline genetic data sets containing major salmon stocks, such as:

- **Chinook baseline** – We coordinated the Pacific Salmon Commission-funded Genetic Analysis of Pacific Salmonids (GAPS) project. This multi-agency project involving 10 West Coast laboratories helped create a standardized, comprehensive coast-wide microsatellite DNA database for Chinook salmon.
- **Coho salmon baseline** – We developed a mid-coast (Southern British Columbia, Oregon and Washington) microsatellite DNA baseline for 84 coho salmon populations, and used this baseline in studies of juvenile coho salmon distributions off the Oregon and Washington coasts.



- **Steelhead baseline** – In collaboration with seven other Columbia River basin and West Coast laboratories we have initiated the Stevan Phelps Allele Nomenclature (SPAN) project, an inter-agency effort to create a shared, standardized genetic baseline for steelhead (and rainbow trout). Our current focus is the Columbia River, but progress is being made for Pacific Rim coverage within a few years.
- **Single nucleotide polymorphism baselines** – Our program has developed SNP markers in Pacific salmon for over 15 years. We have a forensic SNP baseline for identifying Endangered Spring-Run Chinook salmon in the Upper Columbia River, and we are participating in a collaboration to augment the GAPS coastwide Chinook microsatellite baseline with standardized SNP markers.

The NWFSC is also using GSI in multiple ecological and forensic applications, including:

- **Oregon/Klamath fisheries project** – We are collaborating with Oregon State University and the Oregon fishery industry (CROOS) on a pilot project to use GSI to evaluate Klamath fall Chinook distributions off the Oregon coast.
- **Studies of salmon ocean distribution** – We have several ongoing GSI projects in collaboration with NWFSC, SWFSC and OSU scientists to study the ocean distributions of juvenile salmon, including coho and Chinook salmon off the California, Oregon and Washington coasts and in the Columbia River plume and estuary.
- **Studies of Puget Sound distribution** – We have an ongoing study in collaboration with other NWFSC investigators to study the early marine distributions of juvenile Chinook salmon.
- **Forensics and prey studies** – We use GSI to identify the stock origin of individual fish of interest for forensic applications in collaboration with the NOAA Office of Law Enforcement, as well as genetic identification of harbor seal and killer whale prey remains.
- **In-river studies** – We have several recent or ongoing GSI studies of temporal distributions of migrating stocks, including Columbia River steelhead, Willamette River Chinook, and White River (Puget Sound) Chinook.

For more GSI information

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Learn more & come see us in action

Sharing our work with other scientists, policymakers, resource managers, and the public is important to us. To learn more about what we do, please visit our website at: www.nwfsc.noaa.gov and follow @NOAA_NWFSC on Twitter. To obtain additional information, please call 206-860-3200.

By using several DNA markers that are highly variable in salmon, scientists can compare DNA between two tissues. The DNA signature, or "fingerprint" can help scientists assign specimens to their population of origin or match two pieces of evidence.

